

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/790,043

DATE: 03/13/97 #2

TIME: 10:20:52

INPUT SET: S16152.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information

(i) APPLICANT: Lonsdale, John
Milner, Peter
Payne, David
Pearson, Stewart

(ii) TITLE OF THE INVENTION: Novel FabI

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 24-JAN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/024845
(B) FILING DATE: 28-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891
(C) REFERENCE/DOCKET NUMBER: GM50005

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-4478

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47 (B) TELEFAX: 610-270-5090
48 (C) TELEX:
49
50

51 (2) INFORMATION FOR SEQ ID NO:1:
52

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 256 amino acids
55 (B) TYPE: amino acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58

59 (ii) MOLECULE TYPE: protein
60

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62

63	Met	Leu	Asn	Leu	Glu	Asn	Lys	Thr	Tyr	Val	Ile	Met	Gly	Ile	Ala	Asn
64	1			5						10					15	
65	Lys	Arg	Ser	Ile	Ala	Phe	Gly	Val	Ala	Lys	Val	Leu	Asp	Gln	Leu	Gly
66				20					25					30		
67	Ala	Lys	Leu	Val	Phe	Thr	Tyr	Arg	Lys	Glu	Arg	Ser	Arg	Lys	Glu	Leu
68			35				40				45					
69	Glu	Lys	Leu	Leu	Glu	Gln	Leu	Asn	Gln	Pro	Glu	Ala	His	Leu	Tyr	Gln
70		50				55					60					
71	Ile	Asp	Val	Gln	Ser	Asp	Glu	Glu	Val	Ile	Asn	Gly	Phe	Glu	Gln	Ile
72	65				70					75					80	
73	Gly	Lys	Asp	Val	Gly	Asn	Ile	Asp	Gly	Val	Tyr	His	Ser	Ile	Ala	Phe
74				85					90					95		
75	Ala	Asn	Met	Glu	Asp	Leu	Arg	Gly	Arg	Phe	Ser	Glu	Thr	Ser	Arg	Glu
76			100					105					110			
77	Gly	Phe	Leu	Leu	Ala	Gln	Asp	Ile	Ser	Ser	Tyr	Ser	Leu	Thr	Ile	Val
78		115				120					125					
79	Ala	His	Glu	Ala	Lys	Lys	Leu	Met	Pro	Glu	Gly	Gly	Ser	Ile	Val	Ala
80		130				135					140					
81	Thr	Thr	Tyr	Leu	Gly	Gly	Glu	Phe	Ala	Val	Gln	Asn	Tyr	Asn	Val	Met
82	145				150					155					160	
83	Gly	Val	Ala	Lys	Ala	Ser	Leu	Glu	Ala	Asn	Val	Lys	Tyr	Leu	Ala	Leu
84			165					170						175		
85	Asp	Leu	Gly	Pro	Asp	Asn	Ile	Arg	Val	Asn	Ala	Ile	Ser	Ala	Gly	Pro
86			180					185					190			
87	Ile	Arg	Thr	Leu	Ser	Ala	Lys	Gly	Val	Gly	Gly	Phe	Asn	Thr	Ile	Leu
88		195				200						205				
89	Lys	Glu	Ile	Glu	Glu	Arg	Ala	Pro	Leu	Lys	Arg	Asn	Val	Asp	Gln	Val
90		210				215					220					
91	Glu	Val	Gly	Lys	Thr	Ala	Ala	Tyr	Leu	Leu	Ser	Asp	Leu	Ser	Ser	Gly
92	225				230					235					240	
93	Val	Thr	Gly	Glu	Asn	Ile	His	Val	Asp	Ser	Gly	Phe	His	Ala	Ile	Lys
94			245					250							255	

96 (2) INFORMATION FOR SEQ ID NO:2:

97 (i) SEQUENCE CHARACTERISTICS:

98 (A) LENGTH: 771 base pairs
99

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100 (B) TYPE: nucleic acid
101 (C) STRANDEDNESS: double
102 (D) TOPOLOGY: linear
103
104 (ii) MOLECULE TYPE: Genomic DNA
105
106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
107
108 ATGTTAAATC TTGAAAACAA AACATATGTC ATCATGGGAA TCGCTAATAA GCGTAGTATT 60
109 GCTTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA AATTAGTATT TACTTACCGT 120
110 AAAGAACGTA GCCGTAAAGA GCTTGAAAAA TTATTAGAAC AATTAAATCA ACCAGAAGCG 180
111 CACTTATATC AAATTGATGT TCAAAGCGAT GAAGAGGTTA TTAATGGTTT TGAGCAAATT 240
112 GGTAAGATG TTGGCAATAT TGATGGTGTA TATCATTCAA TCGCATTTCG TAATATGGAA 300
113 GACTTACGCG GACGCTTTTC TGAACTTCA CGTGAAGGCT TCTTGTTAGC TCAAGACATT 360
114 AGTTCCTTACT CATTAAACAAT TGTGGCTCAT GAAGCTAAAA AATTAATGCC AGAAGGTGGT 420
115 AGCATTGTTG CAACAACATA TTTAGGTGGC GAATTCGCAG TTCAAAATTA TAATGTGATG 480
116 GGTGTTGCTA AAGCGAGCTT AGAAGCAAAT GTTAAATATT TAGCATTAGA CTTAGGTCCT 540
117 GATAATATTC GCGTTAATGC AATTTAGCT GGTCCAATCC GTACATTAAG TGCAAAAGGT 600
118 GTGGGTGGTT TCAATACAAT TCTTAAAGAA ATCGAAGAGC GTGCACCTTT AAAACGTAAC 660
119 GTTGATCAAG TAGAAGTAGG TAAAACAGCG GCTTACTTTR TAAGTGACTT ATCAAGTGGC 720
120 GTTACAGGTG AAAATATTCA TGTAGATAGC GGATTCCACG CAATTAAATA A 771

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SEQUENCE VERIFICATION REPORT

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Line

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Original Text